STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: 10/572,348

Source: JFWP

Date Processed by STIC: 02/08/2007

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER
VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
     http://www.uspto.gov/web/offices/pac/checker/chkruote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the
United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>, **EFS Submission
   User Manual - ePAVE)**
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
   U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street,
   Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/572,348

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics / Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ____ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ____ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length — Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ____ Skipped Sequences (OLD RULES) — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences (NEW RULES) — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ Invalid <213> Response — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

11 ____ Use of <220> — Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

12 ____ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n/Xaa — "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC – STIC Systems Branch – 03/02/06

IFWP

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/572,348

DATE: 02/08/2007
TIME: 11:42:29

Input Set : A:\sequence listing.txt
Output Set: N:\CRF4\02082007\J572348.raw

```
  3 <110> APPLICANT: Novo Nordisk A/S
  5 <120> TITLE OF INVENTION: Novel GLP-1 derivatives
  7 <130> FILE REFERENCE: 6692-WO
C-->  9 <140> CURRENT APPLICATION NUMBER: US/10/572,348
C-->  9 <141> CURRENT FILING DATE: 2006-03-17
  9 <160> NUMBER OF SEQ ID NOS: 5
 11 <170> SOFTWARE: PatentIn version 3.1
 13 <210> SEQ ID NO: 1
 14 <211> LENGTH: 31
 15 <212> TYPE: PRT
 16 <213> ORGANISM: Homo sapiens
 18 <400> SEQUENCE: 1
 20 His Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly
 21 1               5                   10                  15
 24 Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly
 25             20                  25                  30
 28 <210> SEQ ID NO: 2
 29 <211> LENGTH: 40
 30 <212> TYPE: PRT
 31 <213> ORGANISM: Synthetic construct
 33 <220> FEATURE:
 34 <221> NAME/KEY: MISC_FEATURE
 35 <222> LOCATION: (1)..(1)
 36 <223> OTHER INFORMATION: Xaa at position 1 is L-histidine, D-histidine, desamino-
histidine
 37      , 2-amino-histidine, beta-hydroxy-histidine, homohistidine, N-alp
 38      ha-acetyl-histidine, alpha-fluoromethyl-histidine, alpha-methyl-h
 39      istidine, 3-pyridylalanine, 2-pyridylalanine, or 4-pyridylalanine
W--> 40      .
 43 <220> FEATURE:
 44 <221> NAME/KEY: MISC_FEATURE
 45 <222> LOCATION: (2)..(2)
 46 <223> OTHER INFORMATION: Xaa at position 2 is Ala, Gly, Val, Leu, Ile, Lys, Aib, (1-
aminoc
 47      yclopropyl) carboxylic acid, (1-aminocyclobutyl) carboxylic acid,
 48      (1-aminocyclopentyl) carboxylic acid, (1-aminocyclohexyl) carboxy
 49      lic acid, (1-aminocycloheptyl) carboxylic acid or (1-aminocyclooc
W--> 50      tyl) carboxylic acid.
 53 <220> FEATURE:
 54 <221> NAME/KEY: MISC_FEATURE
 55 <222> LOCATION: (10)..(10)
 56 <223> OTHER INFORMATION: Xaa at position 10 is Val or Leu.
 59 <220> FEATURE:
 60 <221> NAME/KEY: MISC_FEATURE
```

Does Not Comply Corrected Diskette Needed
Cpg-1,5,6)

? Invalid Response.
∟213? Responses are Artificial,
Unknown or Genus Species.
Pls See Item 10 on Error Summary Sheet.

61. <222> LOCATION: (12)..(12)

```
62 <223> OTHER INFORMATION: Xaa at position 12 is Ser, Lys or Arg.
65 <220> FEATURE:
66 <221> NAME/KEY: MISC_FEATURE
67 <222> LOCATION: (13)..(13)
68 <223> OTHER INFORMATION: Xaa at position 13 is Tyr or Gln.
71 <220> FEATURE:
72 <221> NAME/KEY: MISC_FEATURE
73 <222> LOCATION: (14)..(14)
74 <223> OTHER INFORMATION: Xaa at position 14 is Leu or Met.
77 <220> FEATURE:
78 <221> NAME/KEY: MISC_FEATURE
79 <222> LOCATION: (16)..(16)
80 <223> OTHER INFORMATION: Xaa at position 16 is Gly, Glu or Aib.
83 <220> FEATURE:
84 <221> NAME/KEY: MISC_FEATURE
85 <222> LOCATION: (17)..(17)
86 <223> OTHER INFORMATION: Xaa at position 17 is Gln, Glu, Lys or Arg.
89 <220> FEATURE:
90 <221> NAME/KEY: MISC_FEATURE
91 <222> LOCATION: (19)..(19)
92 <223> OTHER INFORMATION: Xaa at position 19 is Ala or Val.
95 <220> FEATURE:
96 <221> NAME/KEY: MISC_FEATURE
97 <222> LOCATION: (20)..(20)
98 <223> OTHER INFORMATION: Xaa at position 20 is Lys, Glu or Arg.
101 <220> FEATURE:
102 <221> NAME/KEY: MISC_FEATURE
103 <222> LOCATION: (21)..(21)
104 <223> OTHER INFORMATION: Xaa at position 21 is Glu or Leu.
107 <220> FEATURE:
108 <221> NAME/KEY: MISC_FEATURE
109 <222> LOCATION: (24)..(24)
110 <223> OTHER INFORMATION: Xaa at position 24 is Ala, Glu or Arg.
113 <220> FEATURE:
114 <221> NAME/KEY: MISC_FEATURE
115 <222> LOCATION: (27)..(27)
116 <223> OTHER INFORMATION: Xaa at position 27 is Val or Lys.
119 <220> FEATURE:
120 <221> NAME/KEY: MISC_FEATURE
121 <222> LOCATION: (28)..(28)
122 <223> OTHER INFORMATION: Xaa at position 28 is Lys, Glu, Asn or Arg.
125 <220> FEATURE:
126 <221> NAME/KEY: MISC_FEATURE
127 <222> LOCATION: (29)..(29)
128 <223> OTHER INFORMATION: Xaa at position 29 is Gly or Aib.
131 <220> FEATURE:
132 <221> NAME/KEY: MISC_FEATURE
133 <222> LOCATION: (30)..(30)
134 <223> OTHER INFORMATION: Xaa at position 30 is Arg, Gly or Lys.
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/572,348

DATE: 02/08/2007
TIME: 11:42:29

Input Set : A:\sequence listing.txt
Output Set: N:\CRF4\02082007\J572348.raw

```
      137 <220> FEATURE:
      138 <221> NAME/KEY: MISC_FEATURE
      139 <222> LOCATION: (31)..(31)
      140 <223> OTHER INFORMATION: Xaa at position 31 is Gly, Ala, Glu, Pro, Lys, amide or is
absent
      141
      144 <220> FEATURE:
      145 <221> NAME/KEY: MISC_FEATURE
      146 <222> LOCATION: (32)..(32)
      147 <223> OTHER INFORMATION: Xaa at position 32 is Lys, Ser, amide or is absent.
      150 <220> FEATURE:
      151 <221> NAME/KEY: MISC_FEATURE
      152 <222> LOCATION: (33)..(33)
      153 <223> OTHER INFORMATION: Xaa at position 33 is Ser, Lys, amide or is absent.
      156 <220> FEATURE:
      157 <221> NAME/KEY: MISC_FEATURE
      158 <222> LOCATION: (34)..(34)
      159 <223> OTHER INFORMATION: Xaa at position 34 is Gly, amide or is absent.
      162 <220> FEATURE:
      163 <221> NAME/KEY: MISC_FEATURE
      164 <222> LOCATION: (35)..(35)
      165 <223> OTHER INFORMATION: Xaa at position 35 is Ala, amide or is absent.
      168 <220> FEATURE:
      169 <221> NAME/KEY: MISC_FEATURE
      170 <222> LOCATION: (36)..(36)
      171 <223> OTHER INFORMATION: Xaa at position 36 is Pro, amide or is absent.
      174 <220> FEATURE:
      175 <221> NAME/KEY: MISC_FEATURE
      176 <222> LOCATION: (37)..(37)
      177 <223> OTHER INFORMATION: Xaa at position 37 is Pro, amide or is absent.
      180 <220> FEATURE:
      181 <221> NAME/KEY: MISC_FEATURE
      182 <222> LOCATION: (38)..(38)
      183 <223> OTHER INFORMATION: Xaa at position 38 is Pro, amide or is absent.
      186 <220> FEATURE:
      187 <221> NAME/KEY: MISC_FEATURE
      188 <222> LOCATION: (39)..(39)
      189 <223> OTHER INFORMATION: Xaa at position 39 is Ser, amide or is absent.
      192 <220> FEATURE:
      193 <221> NAME/KEY: MISC_FEATURE
      194 <222> LOCATION: (40)..(40)
      195 <223> OTHER INFORMATION: Xaa at position 40 is amide or is absent.
      198 <400> SEQUENCE: 2
W--> 200 Xaa Xaa Glu Gly Thr Phe Thr Ser Asp Xaa Ser Xaa Xaa Xaa Glu Xaa
      201 1               5                   10              15
      204 Xaa Ala Xaa Xaa Xaa Phe Ile Xaa Trp Leu Xaa Xaa Xaa Xaa Xaa Xaa
      205                 20                  25              30
      208 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
      209             35                  40
      212 <210> SEQ ID NO: 3
```

RAW SEQUENCE LISTING   DATE: 02/08/2007
PATENT APPLICATION: US/10/572,348   TIME: 11:42:29

Input Set : A:\sequence listing.txt
Output Set: N:\CRF4\02082007\J572348.raw

```
    213 <211> LENGTH: 32
    214 <212> TYPE: PRT                            → Same Error
    215 <213> ORGANISM: (Synthetic construct)
    217 <220> FEATURE:
    218 <221> NAME/KEY: MISC_FEATURE
    219 <222> LOCATION: (1)..(1)
    220 <223> OTHER INFORMATION: Xaa at position 1 is L-histidine, D-histidine, desamino-
histidine
    221         , 2-amino-histidine, beta-hydroxy-histidine, homohistidine, N-alp
    222         ha-acetyl-histidine, alpha-fluoromethyl-histidine, alpha-methyl-h
    223         istidine, 3-pyridylalanine, 2-pyridylalanine, or 4-pyridylalanine
W--> 224         .
    227 <220> FEATURE:
    228 <221> NAME/KEY: MISC_FEATURE
    229 <222> LOCATION: (2)..(2)
    230 <223> OTHER INFORMATION: Xaa at position 2 is Ala, Gly, Val, Leu, Ile, Lys, Aib, (1-
aminoc
    231         yclopropyl) carboxylic acid, (1-aminocyclobutyl) carboxylic acid,
    232         (1-aminocyclopentyl) carboxylic acid, (1-aminocyclohexyl) carboxy
    233         lic acid, (1-aminocycloheptyl) carboxylic acid or (1-aminocyclooc
W--> 234         tyl) carboxylic acid.
    237 <220> FEATURE:
    238 <221> NAME/KEY: MISC_FEATURE
    239 <222> LOCATION: (12)..(12)
    240 <223> OTHER INFORMATION: Xaa at position 12 is Ser, Lys or Arg.
    243 <220> FEATURE:
    244 <221> NAME/KEY: MISC_FEATURE
    245 <222> LOCATION: (16)..(16)
    246 <223> OTHER INFORMATION: Xaa at position 16 is Gly, Glu or Aib.
    249 <220> FEATURE:
    250 <221> NAME/KEY: MISC_FEATURE
    251 <222> LOCATION: (17)..(17)
    252 <223> OTHER INFORMATION: Xaa at position 17 is Gln, Gly, Lys or Arg.
    255 <220> FEATURE:
    256 <221> NAME/KEY: MISC_FEATURE
    257 <222> LOCATION: (20)..(20)
    258 <223> OTHER INFORMATION: Xaa at position 20 is Lys, Glu or Arg.
    261 <220> FEATURE:
    262 <221> NAME/KEY: MISC_FEATURE
    263 <222> LOCATION: (24)..(24)
    264 <223> OTHER INFORMATION: Xaa at position 24 is Ala, Glu or Arg.
    267 <220> FEATURE:
    268 <221> NAME/KEY: MISC_FEATURE
    269 <222> LOCATION: (28)..(28)
    270 <223> OTHER INFORMATION: Xaa at position 28 is Lys, Glu or Arg.
    273 <220> FEATURE:
    274 <221> NAME/KEY: MISC_FEATURE
    275 <222> LOCATION: (29)..(29)
    276 <223> OTHER INFORMATION: Xaa at position 29 is Gly or Aib.
    279 <220> FEATURE:
    280 <221> NAME/KEY: MISC_FEATURE
```

RAW SEQUENCE LISTING   DATE: 02/08/2007
PATENT APPLICATION: US/10/572,348   TIME: 11:42:29

                    Input Set : A:\sequence listing.txt
                    Output Set: N:\CRF4\02082007\J572348.raw

```
281 <222> LOCATION: (30)..(30)
282 <223> OTHER INFORMATION: Xaa at position 30 is Arg or Lys..
285 <220> FEATURE:
286 <221> NAME/KEY: MISC_FEATURE
287 <222> LOCATION: (31)..(31)
288 <223> OTHER INFORMATION: Xaa at position 31 is Gly, Ala, Glu or Lys.
291 <220> FEATURE:
292 <221> NAME/KEY: MISC_FEATURE
293 <222> LOCATION: (32)..(32)
294 <223> OTHER INFORMATION: Xaa at position 32 is Lys, amide or is absent.
297 <400> SEQUENCE: 3
```
W--> 299 Xaa Xaa Glu Gly Thr Phe Thr Ser Asp Val Ser Xaa Tyr Leu Glu Xaa
     300 1   5   10   15
```
303 Xaa Ala Ala Xaa Glu Phe Ile Xaa Trp Leu Val Xaa Xaa Xaa Xaa Xaa
304            20           25              30
307 <210> SEQ ID NO: 4
308 <211> LENGTH: 39
309 <212> TYPE: PRT
310 <213> ORGANISM: Gila monster
312 <220> FEATURE:
313 <221> NAME/KEY: MISC_FEATURE
314 <222> LOCATION: (39)..(39)
315 <223> OTHER INFORMATION: Amidation of carboxy group.
318 <400> SEQUENCE: 4
320 His Gly Glu Gly Thr Phe Thr Ser Asp Leu Ser Lys Gln Met Glu Glu
321 1               5                   10                  15
324 Glu Ala Val Arg Leu Phe Ile Glu Trp Leu Lys Asn Gly Gly Pro Ser
325            20              25              30
328 Ser Gly Ala Pro Pro Pro Ser
329         35
332 <210> SEQ ID NO: 5
333 <211> LENGTH: 44
334 <212> TYPE: PRT
335 <213> ORGANISM: Synthetic construct
337 <220> FEATURE:
338 <221> NAME/KEY: MISC_FEATURE
339 <222> LOCATION: (44)..(44)
340 <223> OTHER INFORMATION: Amidation of carboxy group.
343 <400> SEQUENCE: 5
345 His Gly Glu Gly Thr Phe Thr Ser Asp Leu Ser Lys Gln Met Glu Glu
346 1               5                   10                  15
349 Glu Ala Val Arg Leu Phe Ile Glu Trp Leu Lys Asn Gly Gly Pro Ser
350            20              25              30
353 Ser Gly Ala Pro Pro Ser Lys Lys Lys Lys Lys Lys
354         35              40
```

→ Same Error (handwritten)

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 02/08/2007
PATENT APPLICATION: US/10/572,348   TIME: 11:42:30

Input Set : A:\sequence listing.txt
Output Set: H:\CRF4\02082007\J572348.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; Xaa Pos. 1,2,10,12,13,14,16,17,19,20,21,24,27,28,29,30,31,32,33,34
Seq#:2; Xaa Pos. 35,36,37,38,39,40
Seq#:3; Xaa Pos. 1,2,12,16,17,20,24,28,29,30,31,32

VERIFICATION SUMMARY   DATE: 02/08/2007
PATENT APPLICATION: US/10/572,348   TIME: 11:42:30

Input Set : A:\sequence listing.txt
Output Set: N:\CRF4\02082007\J572348.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:40 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:50 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:200 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
M:341 Repeated in SeqNo=2
L:224 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:234 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:299 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
M:341 Repeated in SeqNo=3